

3. (Amended) The method of Claim 1 wherein said non-coding region [intron] sequence is adjacent to an exon encoding said allele.

6. (Amended) The method of Claim 5 wherein said amplified DNA sequence includes at least about 1,000 nucleotides corresponding to non-coding region [intron] sequences.

7. (Amended) A method for detection of at least one allele of a multi-allelic genetic locus comprising:

- a) amplifying genomic DNA with a [an intron-spanning] primer pair that spans a non-coding region sequence, said primer pair defining [that defines] a DNA sequence which is [, said DNA sequence being] in genetic linkage with said allele and contains [containing] a sufficient number of non-coding region [intron] sequence nucleotides to produce an amplified DNA sequence characteristic of said allele; and
- b) analyzing said amplified DNA sequence to detect the presence of a genetic variation in said amplified sequence.

15. (Amended) The method of Claim 7 wherein at least about 70% of said primer-defined amplified DNA sequence corresponds to non-coding region [intron] sequences.

17. (Amended) A method for producing RFLP fragments characteristic of alleles of [for] an HLA locus of an individual comprising the steps of:

- a) amplifying genomic HLA DNA from said individual with a primer pair specific for said HLA locus under conditions suitable to produce an amplified DNA sequence; and
- b) producing a digest by combining said amplified DNA sequence with at least one endonuclease that cleaves said amplified DNA sequence to yield a set of fragments having distinctive fragment lengths.

Add the following new claims.

- 35 34. The method of Claim 1 wherein said genetic locus has at least four alleles.
- 36 35. The method of Claim 1 wherein said genetic locus has at least eight alleles.
- 37 36. An improved DNA analysis method in which coding region alleles of a multi-allelic genetic locus are determined by identifying sequence polymorphisms characteristic of the alleles, the improvement comprising identifying sequence polymorphisms characteristic of the alleles in a non-coding region sequence, said non-coding region sequence being not more than about two kilobases in length.
- 38 37. The method of Claim 36 wherein said non-coding region sequence is not more than about one kilobase in length.
- 39 38. The method of Claim 36 wherein said sequence polymorphisms characteristic of the alleles are within five kilobases of a variable exon of the genetic locus.
- 40 39. The method of Claim 36 wherein said sequence polymorphisms characteristic of the alleles are within two kilobases of a variable exon of the genetic locus.
- 41 40. The method of Claim 36 wherein said sequence polymorphism characteristic of said coding region allele is present in an intervening sequence adjacent to a variable exon of the locus.
- 42 41. The method of Claim 40 wherein the genetic locus is an HLA Class I locus and the intervening sequence is intervening sequence I, II or III.
- 43 42. The method of Claim 40 wherein the genetic locus is an HLA Class II locus and the intervening sequence is intervening sequence I or II.